```
1     AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA   59
                                                          MetPro      2

60    AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC  119
3     ArgGluAspAlaHisPheIleTyrGlyTyr ProLysLysGlyHisGlyHisSerTyrThr   22

120   ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC  180
23    ThrAlaGluGluAlaAlaGlyIleGlyIle LeuThrValIleLeuGlyValLeuLeuLeu   43

181   ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT  239
44    IleGlyCysTrpTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu   62

240   CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG  300
63    HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGluGlyPheAspHisArg   83

301   GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT  359
84    AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro  102

360   GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG  420
103   AlaTyrGluLysLeuSerAlaGluGlnSer ProProProTyrSerPro              118

421   AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC  479
```

FIG. 1A

```
 480   ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC   540
 541   AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA   599
 600   TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA   660
 661   GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT   719
 720   GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG   780
 781   AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG   839
 840   GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT   900
 901   CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC   959
 960   CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG  1020
1021   GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG  1079
1080   CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT  1140
1141   AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA  1199
1200   TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT  1260
1261   GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC  1319
1320   AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT  1380
1381   AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG  1439
1440   TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG  1500
1501   AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAA  1559
```

FIG. 1B

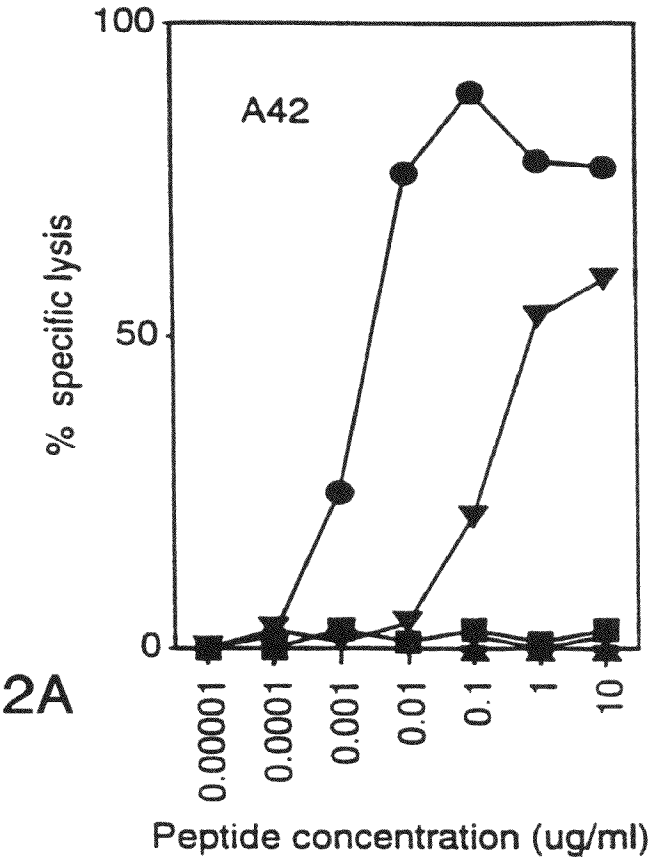
100
A42
% specific lysis
50
0
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2A

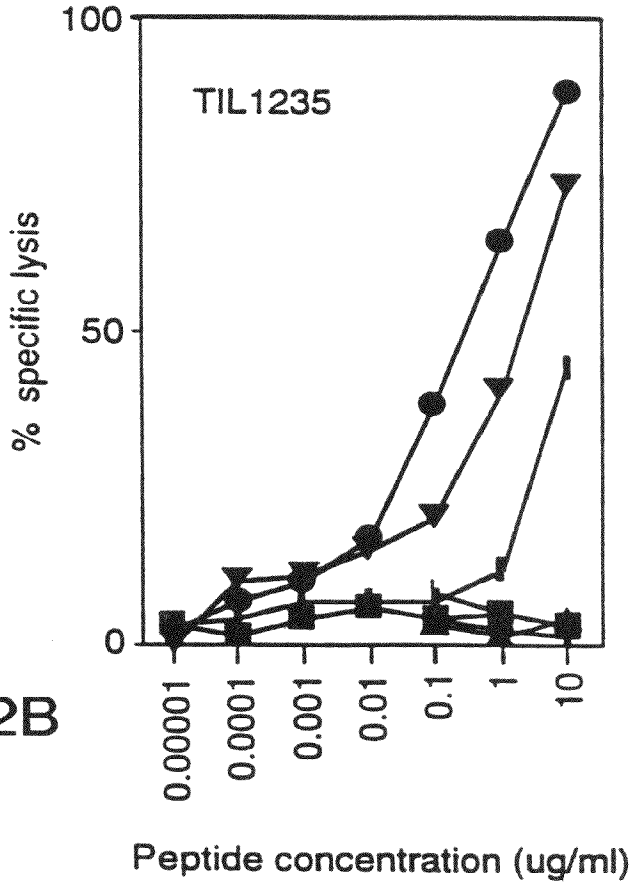
100
TIL1235
% specific lysis
50
0
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2B

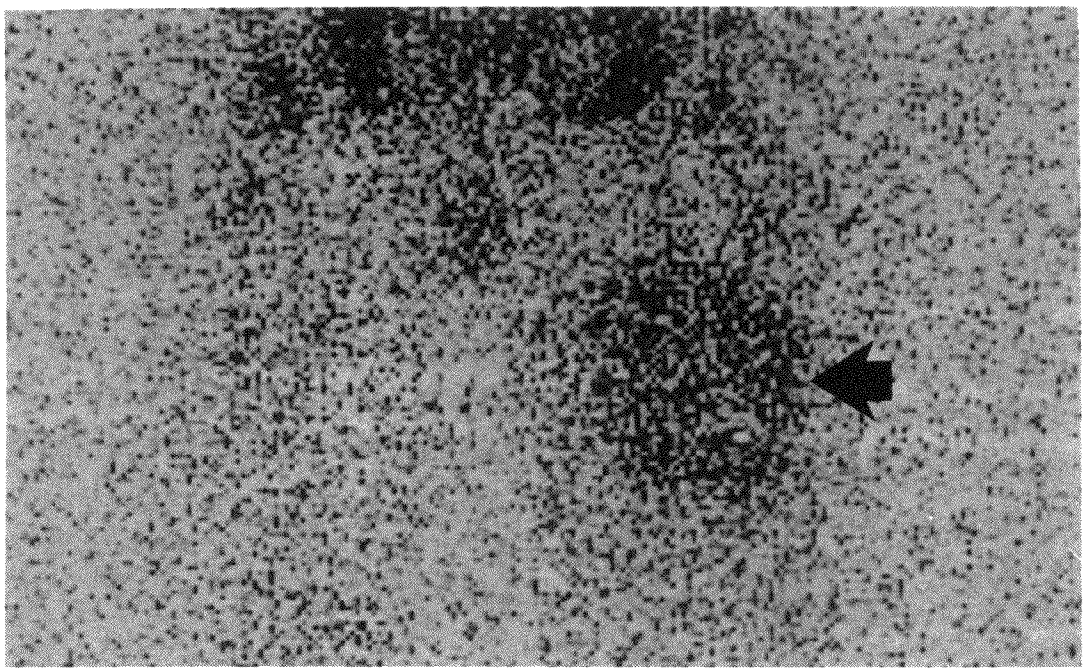

FIG. 3A

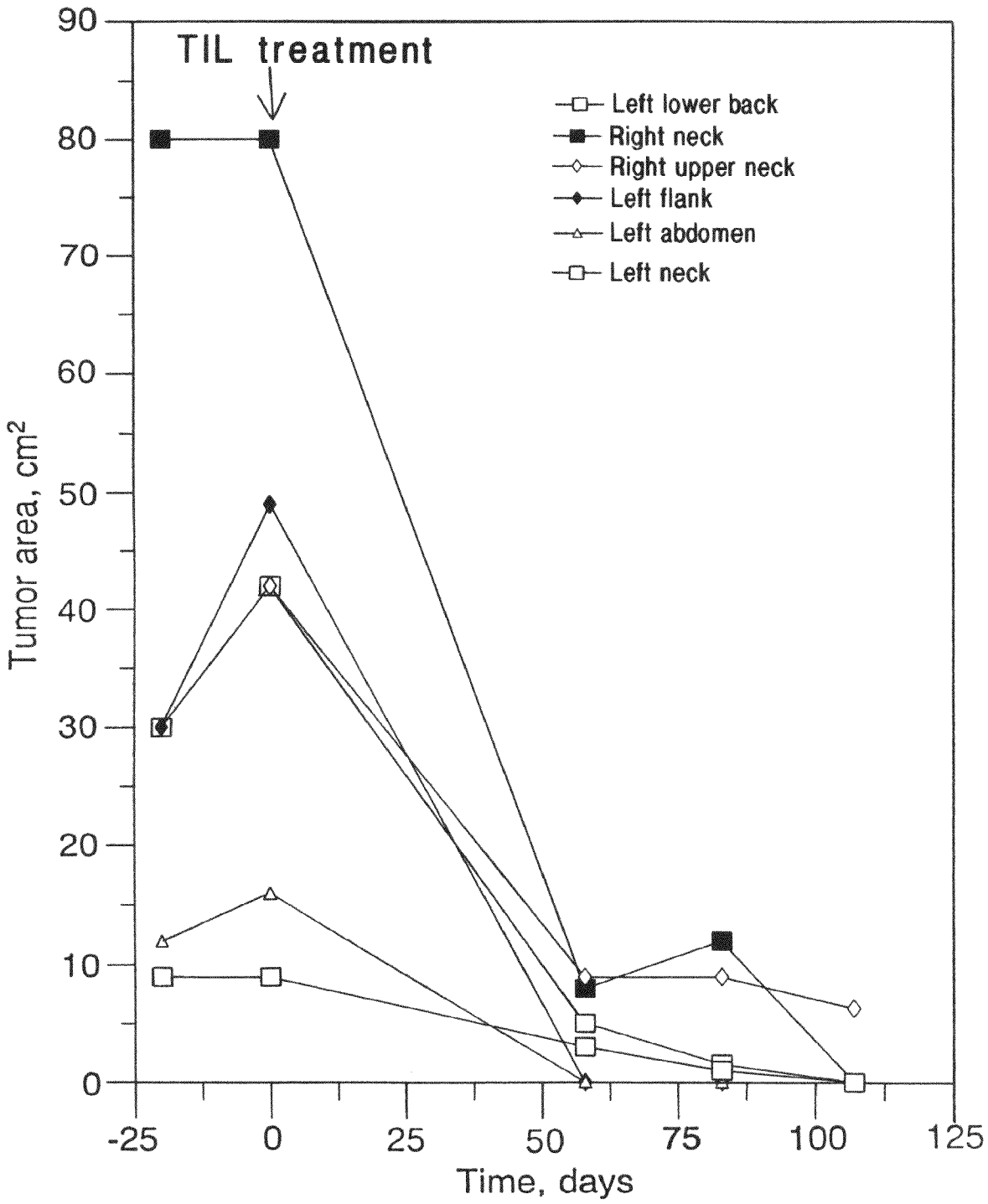
TIL treatment
Left lower back
Right neck
Right upper neck
Left flank
Left abdomen
Left neck
Tumor area, cm2
Time, days
90
80
70
60
50
40
30
20
10
0
-25
0
25
50
75
100
125

FIG. 3B

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40

GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80

ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120

GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160

CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200

GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240

TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA 280

TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA 320

AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA 360

CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT 400

GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440

GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480

GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA 520

ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA 560

GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG 600

TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640

TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680

TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG 720

GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC 760

CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT 800

GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840

CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880

GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920

GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960

GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA 1000

CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT 1040

ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA 1080

CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120

FIG. 4A

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG 1160

ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA 1200

CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC 1240

ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA 1280

GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG 1320

CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC 1360

CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG 1400

GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA 1440

AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG 1480

TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA 1520

AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG 1560

ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC 1600

CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG 1640

CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC 1680

CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG 1720

CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC 1760

AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG 1800

GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG 1840

CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG 1880

ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC 1920

CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC 1960

CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC 2000

CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG 2040

CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC 2080

CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT 2120

ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA 2160

AAAAAAAAAA AA 2172

FIG. 4B

```
  1   MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
 51   EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
101   QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151   YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201   AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251   LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301   CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351   VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401   TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451   TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501   AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC
551   QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601   GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651   ENSPLLSGQQ V
```

FIG. 5A

```
Pmel17      M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20        M-----V-----Q-----L-----  .....------------
gp100       M-----V-----Q-----L-----.....--------------
cDNA25FL    M-----F-----Q-----L-----.....--------------
cDNA25TR                  Q-----L----------------PPQWAAGLSTLI
            1     162    236    274    588           649
```

FIG. 5B

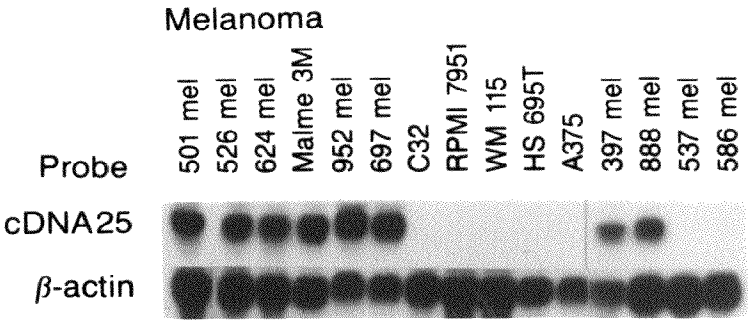

FIG. 6A

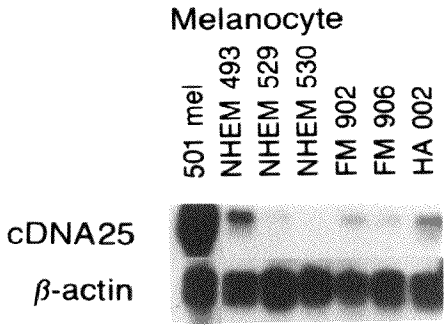

FIG. 6B

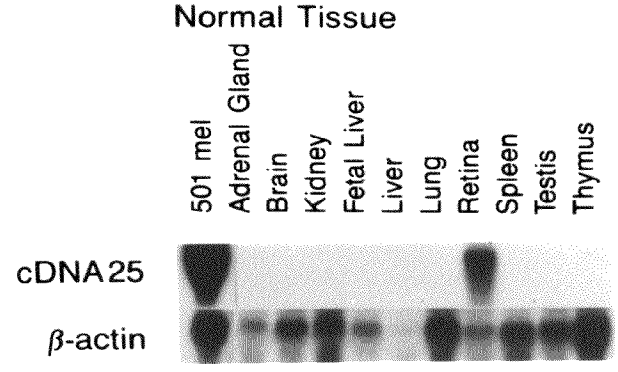

FIG. 6C